

5'	9	18	27	36	45	54
	GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CGG					
	CGG TGG GAA ATG CTG GCG CGC GCG CGG GGG CAC TGG GGC CCT TTT GCT GAG					
	M L A R A A R G H W G P F A E					
	117	126	135	144	153	162
	GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC CGC GCC TCC TCT GGA TTG CCC					
	G L S T G F W P R S G R A S S G L P					
	171	180	189	198	207	216
	CGA AAC ACC GTG GTA CTG TTC GTG CCG CAG CAG GAG GCC TGG GTG GTG GAG CGA					
	R N T V V L F V P Q Q E A W V V E R					
	225	234	243	252	261	270
	ATG GGC CGA TTC CAC CGG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG					
	M G R F H R I L E P G L N I L I P V					
	279	288	297	306	315	324
	TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT					
	L D R I R Y V Q S L K E I V I N V P					
	333	342	351	360	369	378
	GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT					
	E Q S A V T L D N V T L Q I D G V L					
	387	396	405	414	423	432
	TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAG GAC CCT GAG					
	Y L R I M D P Y K A S Y G V E D P E					
	441	450	459	468	477	486
	TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC					
	Y A V T Q L A Q T T M R S E L G K L					
	495	504	513	522	531	540
	TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT					
	S X D K V F R E R E S L N A S I V D					
	549	558	567	576	585	594
	GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC					
	A I N Q A A D C W G I R C L R Y E I					
	603	612	621	630	639	648
	AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG					
	K D I H V P P R V K E S M Q M Q V E					
	657	666	675	684	693	702
	GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT GAG GGG ACC CGA GAG TCG					
	A E R R K R A T V L E S E G T R E S					

FIGURE 1A

711	720	729	738	747	756
GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA					
A I N V A E G K K Q A Q I L A S E A					
-					
765	774	783	792	801	810
GAA AAG GCT GAA CAG ATA AAT CAG GCA GCA GGA GAG GCC AGT GCA GTT CTG GCG					
E K A E Q I N Q A A G E A S A V L A					
-					
819	828	837	846	855	864
AAG GCC AAG GCT AAA GCT GAA GCT ATT CGA ATC CTG GCT GCA GCT CTG ACA CAA					
K A K A K A E A I R I L A A A L T Q					
-					
873	882	891	900	909	918
CAT AAT GGA GAT GCA GCA GCT TCA CTG ACT GTG GCC GAG CAG TAT GTC AGC GCG					
H N G D A A A S L T V A E Q Y V S A					
-					
927	936	945	954	963	972
TTC TCC AAA CTG GCC AAG GAC TCC AAC ACT ATC CTA CTG CCC TCC AAC CCT GGC					
F S K L A K D S N T I L L P S N P G					
-					
981	990	999	1008	1017	1026
GAT GTC ACC AGC ATG GTG GCT CAG GCC ATG GGT GTA TAT GGA GCC CTC ACC AAA					
D V T S M V A Q A M G V Y G A L T K					
-					
1035	1044	1053	1062	1071	1080
GCC CCA GTG CCA GGG ACT CCA GAC TCA CTC TCC AGT GGG AGC AGC AGA GAT GTC					
A P V P G T P D S L S S G S S R D V					
-					
1089	1098	1107	1116	1125	1134
CAG GGT ACA GAT GCA AGT NTT GAT GAG GAA CTT GAT CGA GTC AAG ATG AGT TAG					
Q G T D A S X D E E L D R V K M S *					
-					
1143	1152	1161	1170	1179	1188
TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT					

FIGURE 1B

1 M L A R A A R G H W G - - - P F A E G L S T G F W P R S - - - - - [G R] 789094
 1 M A E K R H T R D S E - - - A - - Q R L P D S E K D S P - - - - - S K GI 31069
 1 M N L K T C S L S T H - - - S F L Q K K N E K H D G N P - - - - - E H GI 1065452
 1 M E Y G M P E G S Y D S V F T Y A P Y N D L D K M G Y M G P A R Q G M M L G N K GI 1353669
 1 M Q G A - Z79701
 1 M -
 28 A S S -
 26 -
 28 Y D T -
 41 Y G N F T Y T R D Y G V N M E D D I K P L S A I E L L I F C V S F L F V [V M T M GI 1353669
 5 -
 9 F -
 41 -
 47 P I S I W M - C I K I I K E Y E R A I I F R L G R I L Q G G A K G P G L F F I L GI 31069
 52 P V S I Y F - C M K V V Q E Y E R A V I F R L G R I L I G G G A K G P G I F F V L GI 1065452
 81 P L S L L F - A L K F I S T S E K L V V L R L G R A Q K - - T R G P G I T L V I GI 1353669
 18 A I I V V A K S V A L I P Q A E A A V V I E R L G R Y S R - - T V S G Q Q L T L V Z79701
 24 -
 68 P V L D R I R Y V O S L K E I V I V N V P E Q S A V T L D N V T L O I D G V L Y L 789094
 86 P C T D S F - I K V D M R T I S F D I P P Q E I L T K D S V T I S V D G V V Y Y GI 31069
 91 P C I E S Y - T K V D L R T V S F S V P P Q E I L T K D S V T T S V D A V I Y Y Y GI 1065452
 118 P C I D T T H - K V T M S I T A F I N V P P L Q I I T T D R G I L V E L G A T V F L GI 1353669
 56 P F I D R V R A R V D L R E R V V S F P P Q P V I T E D N L T L N I D T V V Y F Z79701
 55 P F I D V P - V K V D M R T R V T D I P P Q E M I T K D N A V V K V D A V V Y Y GI 1591514
 108 R I M D P Y K A S X G V E D P E Y A V T O L A Q T T M R S E L G K L S X D K V F 789094
 125 R V O N A T L A V A N I T N A D S A T R L L A Q T T L R N V L G T K N L S Q I L GI 31069
 130 R I S N A T V S V A N V E N A H H S T R L L A Q T T L R N M L G T R S L S E I L GI 1065452
 157 K I R D P I A A V C G V Q D R N A S V R T L A N T M L Y R Y I S K K R I C D V T GI 1353669
 96 Q V T V D Q A A V Y E I S N Y I V G V E Q L T T T L R N V V G G M T L E Q T L Z79701
 94 R V I D V E K A I L E V E D Y E Y A N I I N L A O T T R A I G S M E L D E V L GI 1591514

FIGURE 2A

148	R	- - E R E S L N A S I V D A I N Q A A D C W G I R C L R Y E I K D I H V P P R	789094
165	S	- - D R E E I A H N M Q S T L D D A T D A W G I K V E R V P V Q G I 31069	
170	S	- - D R E T I A S M Q T I L D E A T E S W G I K V E R V P V Q G I 31069	
197	S S Q D P R R I I S A N L K D E L G S F T C Q F G V E I T D V E I S D V K I - - - G I 1065452		
136	T	- - S R D Q I N A Q L R G V L D E A T G R W G L R V A R V E L R S I D D P P P S Z 79701	
134	N	- - K R E Y I N S K L L E I L D R E T D A W G V R I E K V E K E I D P P E D G I 1591514	
186	V K E S M O M O V E A E R K R A T V L E S E G T R E S A I N V A E G K K Q O A Q	789094	
203	L Q R A M A A E A E A S R E A R A K V I A A E G M N A - - - - -		
208	L Q R A M A A E A E A E A T R E A R A K V I A A E G E Q K A - - - - -		
234	V K E G E N M G M S A - - - - -		
174	I Q A S M E K Q M K A D R E K R A M I L T A E G T R E A A T K Q A E G Q K Q O A Q	Z 79701	
172	I K N A M A Q Q M K A E R L K R A A I L E A E G E K P E	G I 1591514	
226	I L A S E A E K A E Q I N O A A G E A S A V L A K A K A E A I - - - - -		
231	- - - - -		
236	- - - - -		
260	V I G P - - - - -		
214	I L I A E G A K Q A A I L A A E A D R Q S R M L R A Q G E R A A A Y L Q A Q G Q	Z 79701	
259	- R I L A A A L T O H N G D A A A S L T V A E Q Y V S A F S K L A K D S N T I I L	789094	
244	- - - - -		
249	- - - - -		
288	S D V P S T S A A G T S T D T P N I P S I D I D H L I S V A S L A M D E H - L V G I 31069		
254	A K A I E K T F A A I K A G R P T P E M I A Y Q Y L Q T L P E M A R G D A N K V	Z 79701	
298	- - - - -		
268	- - - - -		
269	- - - - -		
327	R L I G R V F Q I N C K D I E P - I C I D L K H G S G S A Y K G T S L - - N P D G I 1065452		
2294	W V V P S D F N A A L Q G E F T R L L G P G E D G V F - R F E P S P V Y E D Q Q P K	Z 79701	

FIGURE 2B

FIGURE 2C

Library	Lib Description	Abun	Pct Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577
TESTNOT03	testis, 37 M	1	0.0557
LIVRNOT02	liver, 32 F	1	0.0515
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418
LVENNOT03	heart, left ventricle, 31 M	1	0.0336
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288
KERANOT01	keratinocytes, neonatal M	1	0.0227
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
PGANNOT01	paraganglia, 46 M	1	0.0159
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150

FIGURE 3